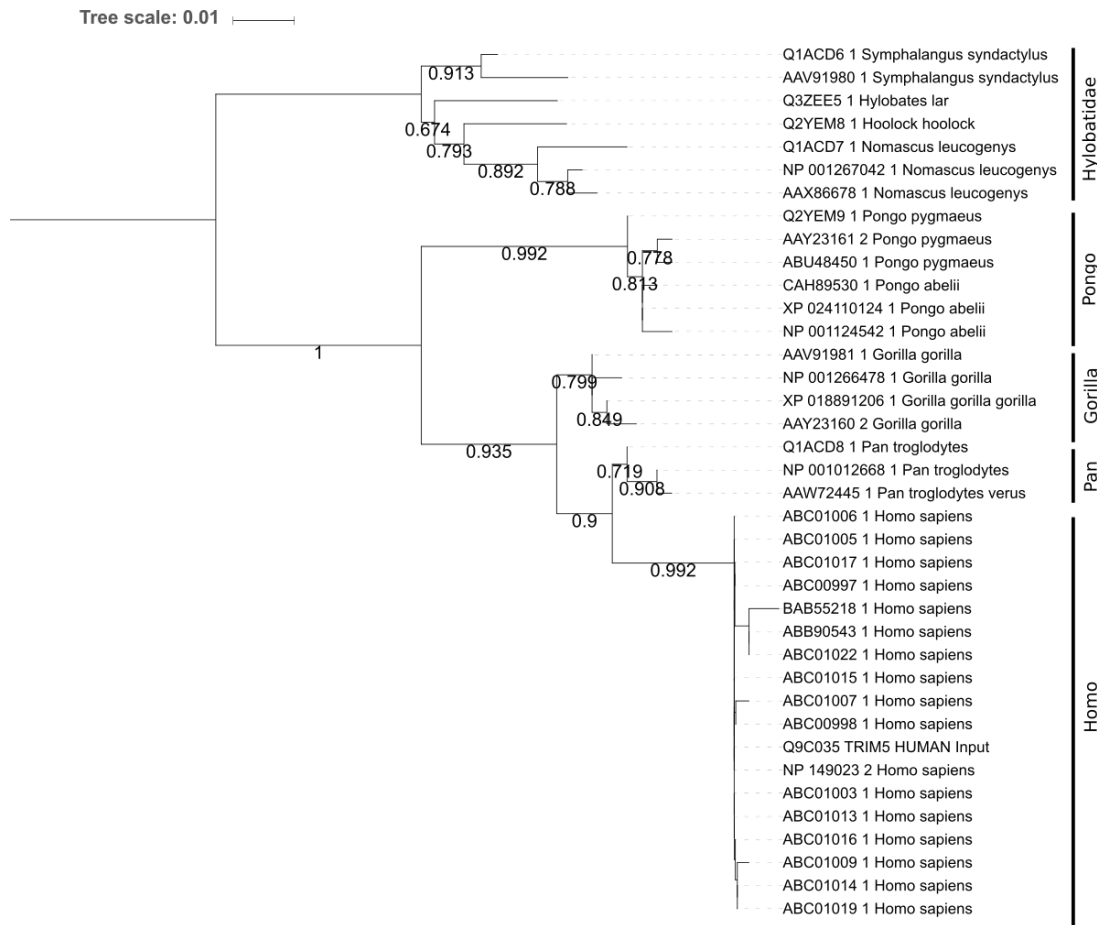# NGPhylogeny.fr: Supplementary material

## Supplementary Figure 1: Trim5 alpha tree inferred with PhyML-SMS

This tree was inferred using the « *Oneclick* » PhyML-SMS workflow, from 38 ape protein sequences. SH-like supports are displayed on every internal branch.

Data have been retrieved using the *Blast-Search* module, from human Trim5 alpha protein sequence (Uniprot id: Q9C035, available as example sequence in *Blast-Search* form), with 'blastp' on 'nrprot' database, a 10^{-5} e.value cutoff and a 80 % query length coverage threshold. Only ape sequences were selected to be analyzed with PhyML-SMS workflow.

The tree represents well the taxonomy of apes, with high branch supports.

All result files are available at https://ngphylogeny.fr/static/Use_Case_data.zip

# Supplementary Figure 2: Trim5 alpha tree inferred with MrBayes
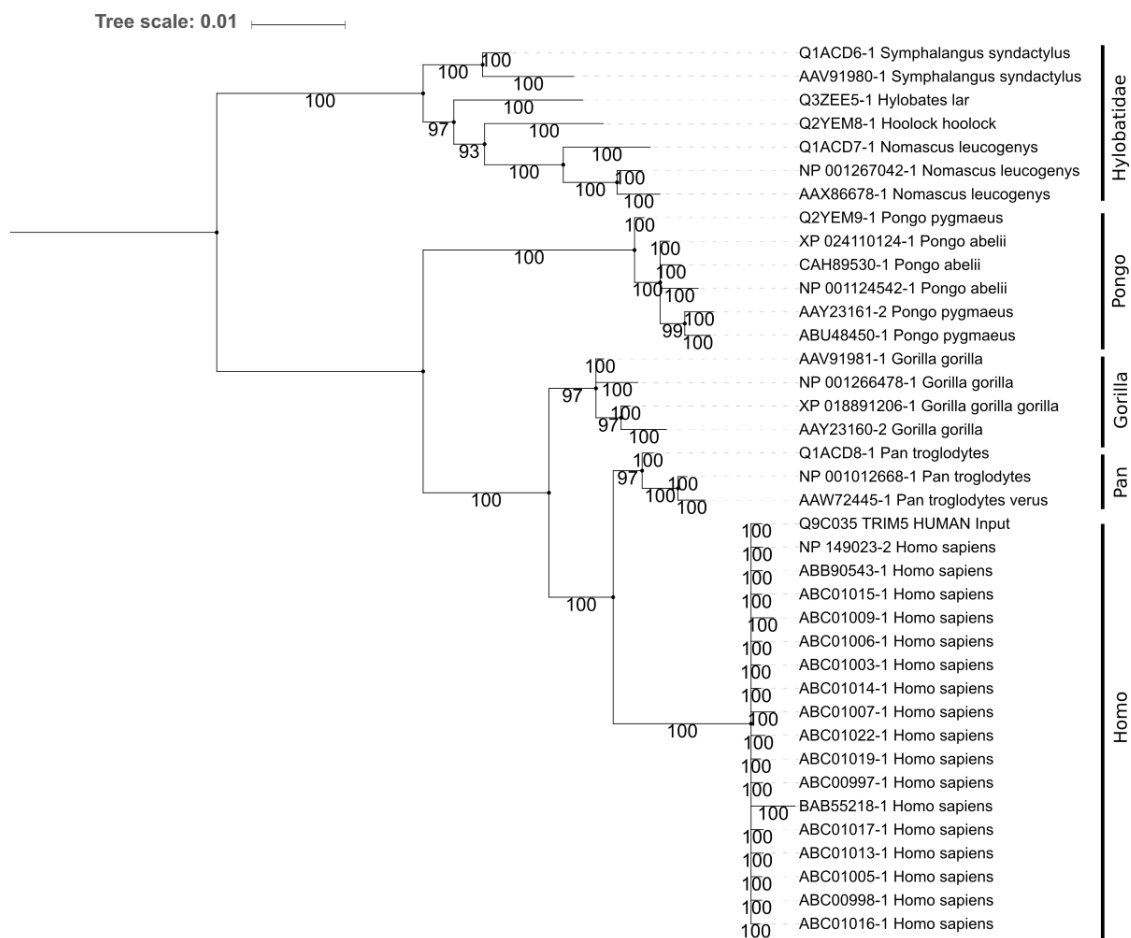
The tree has been inferred using an «*A la carte*» workflow made of MAFFT, BMGE, and MrBayes steps, from the same 38 ape sequences as Supp. Fig.1. Posteriors are shown on every internal branch.

The tree represents well the taxonomy of apes, with high branch supports. The topology is the same highy similar to that obtained using PhyML-SMS (Sup. Fig. 2): all branches inferred by MrBayes are present in the PhyML-SMS tree, but MrBayes tree is not fully resolved.

All result files are available at https://ngphylogeny.fr/static/Use_Case_data.zip

Supplementary Figure 3: HIV pol gene inferred with FastTree and 100 bootstrap replicates
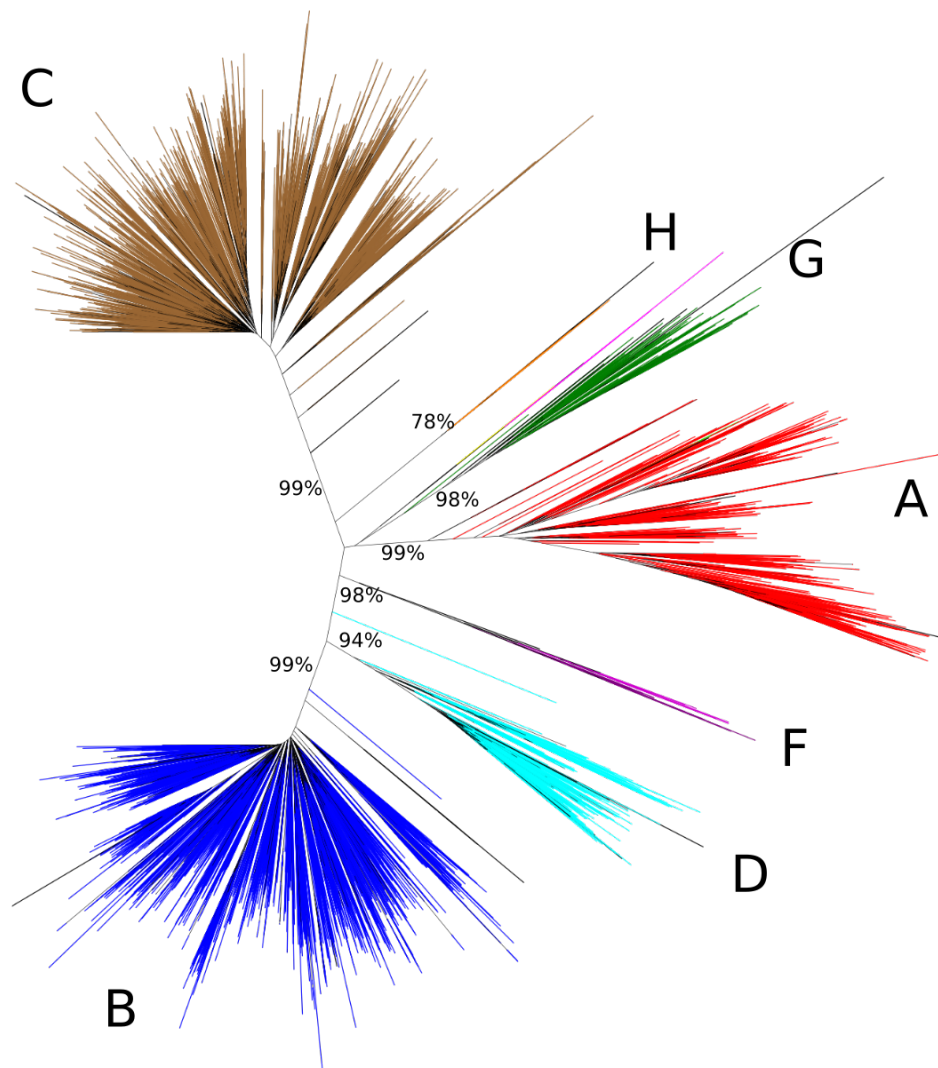
Tree of ~9,150 HIV pol gene sequences[1] analyzed with an « *A la carte* » workflow consisting of MAFFT and FastTree steps. FastTree was configured with nucleotide input sequences and 100 bootstrap replicates[2]. This obtained was obtained in ~8 hours..

Sequences belonging to the same HIV subtypes (colored using JPHMM) are grouped together (with rare exceptions) in the same subtrees, which are highly supported by TBE (see reference (7) for details).

All result files are available at https://ngphylogeny.fr/static/Use_Case_data.zip

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1   https://ngphylogeny.fr/static/hiv_pol.fa.zip
2   https://ngphylogeny.fr/static/hiv_pol_boot_trees.nw.zip